

CLAIMS

What is claimed is:

- 1 1. A method for detecting a polymer in a mixture, the method comprising the
2 computer-implemented steps of:
3 generating both a first mass based on a first version of the polymer that includes a
4 first isotope of an element and a second mass based on a second version of the
5 polymer that includes a second isotope of the element;
6 receiving data based on a mass analysis of the mixture; and
7 determining whether the data indicates an occurrence of a mass doublet that is
8 associated with both the first mass and the second mass.
- 1 2. The method of Claim 1, wherein the polymer is a biopolymer.
- 1 3. The method of Claim 2, wherein the biopolymer is comprised of one or more amino
2 acids.
- 1 4. The method of Claim 2, wherein the biopolymer is comprised of one or more
2 nucleotides.
- 1 5. The method of Claim 1, wherein the mass analysis is a mass spectrographic analysis.
- 1 6. The method of Claim 1, wherein the polymer is a particular polymer of a plurality of
2 polymers, and wherein the method further comprises the computer-implemented steps
3 of:
4 for each polymer of the plurality of polymers, performing the steps of generating and
5 determining.
- 1 7. The method of Claim 6, wherein the plurality of polymers is identified in a library,
2 and wherein the method further comprises the computer-implemented steps of:

receiving one or more length values; and
based on the one or more length values, generating the library of polymers based on
possible fragments of a parent polymer that have lengths corresponding to the
one or more length values.

8. The method of Claim 7, wherein the parent polymer is a protein and the possible
fragments are peptides.

9. The method of Claim 7, wherein the parent polymer is selected from the group
consisting of deoxyribonucleic acid and ribonucleic acid and the possible fragments
are nucleic acids.

10. The method of Claim 1, wherein the element is chosen from the group consisting of
hydrogen, carbon, nitrogen, sulfur, and phosphorous.

11. The method of Claim 1, wherein the element is hydrogen, the first isotope is
hydrogen-1, and the second isotope is hydrogen-2.

12. The method of Claim 1, wherein the element is carbon, the first isotope is carbon-12,
and the second isotope is carbon-13.

13. The method of Claim 1, wherein the element is nitrogen, the first isotope is
nitrogen-14, and the second isotope is nitrogen-15.

14. The method of Claim 1, wherein the step of determining whether the data indicates
the occurrence of the mass doublet is based on input from a user.

15. The method of Claim 1, wherein the step of determining whether the data indicates
the occurrence of the mass doublet comprises the computer-implemented steps of:

3 determining whether the data indicates that the mixture includes both the first version
4 of the polymer and the second version of the polymer;
5 determining whether both a first amount of the first version and a second amount of
6 the second version satisfy a first condition;
7 determining whether a ratio of the first amount to the second amount satisfies a
8 second condition; and
9 determining that the data indicates the occurrence of the mass doublet when the data
10 indicates that the mixture includes both the first version and the second
11 version, the first amount and the second amount satisfy the first condition, and
12 the ratio satisfies the second condition.

1 16. The method of Claim 15, wherein the first amount and the second amount satisfy the
2 first condition when the first amount and the second amount exceed a threshold
3 amount.

1 17. The method of Claim 15, wherein the ratio satisfies the second condition when the
2 ratio is within a range based on a specified ratio and a specified error.

1 18. The method of Claim 1, wherein the data is based on multiple scans of a
2 chromatogram of the mixture, and wherein the step of determining whether the data
3 indicates an occurrence of the mass doublet comprises the computer-implemented
4 steps of:
5 identifying, for each scan of a plurality of the multiple scans, whether the data
6 indicates the occurrence of the mass doublet; and
7 if the data for a scan indicates the occurrence of the mass doublet, then generating a
8 first value for said scan.

- 1 19. The method of Claim 18, wherein the first value is based on a first abundance of the
2 first version and a second abundance of the second version.
- 1 20. The method of Claim 18, wherein the step of determining whether the data indicates
2 an occurrence of the mass doublet further comprises the computer-implemented steps
3 of:
4 determining a number of consecutive scans of the plurality of the multiple scans for
5 which a first value is generated; and
6 if the number of consecutive scans satisfies a specified condition, generating a second
7 value.
- 1 21. The method of Claim 20, wherein the step of determining whether the data indicates
2 an occurrence of the mass doublet further comprises the computer-implemented step
3 of:
4 if the data indicates the occurrence of the mass doublet, associating the second value
5 with the polymer.
- 1 22. The method of Claim 20, wherein the number of consecutive scans satisfies the
2 specified condition when the number of consecutive scans is at least as great as a
3 specified number of scans.
- 1 23. The method of Claim 20, wherein the second value is based on the first values that
2 are associated with the number of consecutive scans.
- 1 24. The method of Claim 20, further comprising the computer-implemented step of:
2 determining a quantity measurement based on the second value.
- 1 25. The method of Claim 1, further comprising the computer-implemented step of:
2 automatically determining a quantity measurement for the polymer.

- 1 26. The method of Claim 25, wherein the quantity measurement is a qualitative
2 measurement.
- 1 27. The method of Claim 25, wherein the quantity measurement is a relative quantity
2 measurement.
- 1 28. The method of Claim 25, wherein the quantity measurement is an absolute quantity
2 measurement
- 1 29. The method of Claim 1, wherein the step of generating both the first mass and the
2 second mass comprises the computer-implemented steps of:
3 calculating the first mass based on a first theoretical mass for the first version of the
4 polymer; and
5 calculating the second mass based on a second theoretical mass for the second version
6 of the polymer.
- 1 30. A method for identifying a polymer in a mixture, the method comprising the
2 computer-implemented steps of:
3 receiving one or more length values for fragments of the polymer;
4 based on the one or more length values, generating a library of fragments of the
5 polymer that have lengths corresponding to the one or more length values; and
6 for each fragment in the library, determining whether said fragment is present in the
7 mixture based on a mass spectrographic analysis of the mixture.
- 1 31. The method of Claim 30, wherein the one or more length values includes a minimum
2 length.
- 1 32. The method of Claim 30, wherein the one or more length values includes a maximum
2 length.

1 33. The method of Claim 30, wherein the one or more length values includes a minimum
2 length and a maximum length.

1 34. The method of Claim 30, wherein the one or more length values includes one or more
2 ranges of lengths.

1 35. The method of Claim 30, wherein the one or more length values includes a one or
2 more specified length values that are received from a user.

1 36. The method of Claim 30, wherein the step of determining includes the computer
2 implemented steps of:
3 for each fragment in the library, generating both a first mass based on the fragment
4 having a first isotope of an element and a second mass based on the fragment
5 having a second isotope of the element;
6 for each fragment in the library, determining whether the mass spectrographic
7 analysis indicates an occurrence of a mass doublet that is associated with both
8 the first mass and the second mass.

1 37. A method for detecting biopolymers in a mixture that includes both natural and
2 labeled versions of the biopolymers, the method comprising the
3 computer-implemented steps of:
4 generating a library for at least one biopolymer, wherein the library includes a
5 plurality of biopolymer fragments based on the at least one biopolymer;
6 determining, for each biopolymer fragment of the plurality of biopolymer fragments,
7 both a first mass based on a natural version of the biopolymer fragment that
8 includes a first isotope of an element and a second mass based on a labeled
9 version of the biopolymer fragment that includes a second isotope of the
10 element;

receiving information based on a mass spectrographic analysis of a chromatogram of the mixture, wherein the information includes data for a plurality of scans of the chromatogram;

identifying, for each scan of the plurality of scans, whether the data indicates an occurrence of one or more mass doublets, wherein each mass doublet of the one or more mass doublets is associated with both the natural version and the labeled version of a particular biopolymer fragment of the plurality of biopolymer fragments;

for each mass doublet that is identified,

generating a first score for each scan;

determining a number of consecutive scans of the plurality of scans for which the first score is generated;

if the number of consecutive scans satisfies a specified condition, generating a second score; and

associating the second score with the particular biopolymer fragment that is associated with the mass doublet.

38. The method of Claim 37, further comprising the computer-implemented steps of:

receiving input that specifies a particular number of scans; and

wherein the number of consecutive scans satisfies the specified condition when the number of consecutive scans is at least as great as the particular number of scans.

39. The method of Claim 37, wherein the step of identifying, for each scan of the plurality of scans, whether the data indicates the occurrence of one or more mass doublets comprises the computer-implemented steps of:

for each mass doublet of the one or more mass doublets,

determining whether the data indicates that the mixture includes both the natural version and the labeled version of the particular biopolymer fragment;
determining whether both a first abundance of the natural version and a second abundance of the labeled version exceed a threshold abundance; and
determining whether a ratio of the first abundance of the natural version to the second abundance of the labeled version is consistent with both a specified ratio and a specified error; and
identifying that the data indicates the occurrence of the mass doublet when the data indicates that the mixture includes both the natural version and the labeled version, the first abundance and the second abundance exceed the threshold abundance, and the ratio is consistent with both the specified ratio and the specified error.

40. The method of Claim 39, further comprising the computer-implemented steps of:
receiving input that specifies a mass/charge accuracy associated with the mass spectrographic analysis; and
wherein the step of determining whether the data indicates that mixture includes both the natural version and the labeled version of the particular biopolymer fragment comprises the computer-implemented step of:
identifying whether a first peak occurs in the data, wherein the first peak is based on the first mass and the mass/charge accuracy;
identifying whether a second peak occurs in the data, wherein the second peak is based on the second mass and the mass/charge accuracy; and

determining that the data indicates that the mixture includes both the natural version and the labeled version of the particular biopolymer fragment when both the first peak and the second peak occur in the data.

41. The method of Claim 37, wherein the step of determining both the first mass based on the natural version of the biopolymer fragment and the second mass based on the labeled version of the biopolymer fragment comprises the computer-implemented steps of:

calculating the first mass based on a first theoretical mass for the natural version of the biopolymer fragment; and
calculating the second mass based on a second theoretical mass for the labeled version of the biopolymer fragment.

42. The method of Claim 41, further comprising the computer-implemented steps of: repeating the steps of calculating the first mass and calculating the second mass for each possible charge state of the biopolymer fragment.

43. The method of Claim 42, further comprising the computer-implemented step of: receiving input that specifies one or more possible charge states of the biopolymer fragment.

44. The method of Claim 37, wherein the step of generating the first score comprises the computer-implemented step of:
calculating the first score as a sum of a first average abundance that corresponds to the first mass and a second average abundance that corresponds to the second mass.

45. The method of Claim 37, wherein the step of generating the second score comprises the computer-implemented step of:

calculating the second score as a summation of each first score associated with each
of the number of consecutive scans.

46. The method of Claim 37, further comprising the computer-implemented step of:
ranking, based on the second score for each biopolymer fragment, the one or more
mass doublets that are identified.

47. The method of Claim 37, further comprising the computer-implemented step of:
displaying a plot as a function of time of both a first abundance of the first mass and a
second abundance of the second mass.

48. A computer-readable medium carrying one or more sequences of instructions for
detecting a polymer in a mixture, wherein execution of the one or more sequences of
instructions by one or more processors causes the one or more processors to perform
the steps of:
generating both a first mass based on a first version of the polymer that includes a
first isotope of an element and a second mass based on a second version of the
polymer that includes a second isotope of the element;
receiving data based on a mass analysis of the mixture; and
determining whether the data indicates an occurrence of a mass doublet that is
associated with both the first mass and the second mass.

49. The computer-readable medium of Claim 48, wherein the polymer is a biopolymer.

50. The computer-readable medium of Claim 49, wherein the biopolymer is comprised of
one or more amino acids.

51. The computer-readable medium of Claim 49, wherein the biopolymer is comprised of
one or more nucleotides.

- 1 52. The computer-readable medium of Claim 48, wherein the mass analysis is a mass
2 spectrographic analysis.
- 1 53. The computer-readable medium of Claim 48, wherein the polymer is a particular
2 polymer of a plurality of polymers, and wherein the computer-readable medium
3 further comprises instructions which, when executed by the one or more processors,
4 cause the one or more processors to carry out the steps of:
5 for each polymer of the plurality of polymers, performing the steps of generating and
6 determining.
- 1 54. The computer-readable medium of Claim 53, wherein the plurality of polymers is
2 identified in a library, and wherein the computer-readable medium further comprises
3 instructions which, when executed by the one or more processors, cause the one or
4 more processors to carry out the steps of:
5 receiving one or more length values; and
6 based on the one or more length values, generating the library of polymers based on
7 possible fragments of a parent polymer that have lengths corresponding to the
8 one or more length values.
- 1 55. The computer-readable medium of Claim 54, wherein the parent polymer is a protein
2 and the possible fragments are peptides.
- 1 56. The computer-readable medium of Claim 54, wherein the parent polymer is selected
2 from the group consisting of deoxyribonucleic acid and ribonucleic acid and the
3 possible fragments are nucleic acids.
- 1 57. The computer-readable medium of Claim 48, wherein the element is chosen from the
2 group consisting of hydrogen, carbon, nitrogen, sulfur, and phosphorous.

- 1 58. The computer-readable medium of Claim 48, wherein the element is hydrogen, the
2 first isotope is hydrogen-1, and the second isotope is hydrogen-2.
- 1 59. The computer-readable medium of Claim 48, wherein the element is carbon, the first
2 isotope is carbon-12, and the second isotope is carbon-13.
- 1 60. The computer-readable medium of Claim 48, wherein the element is nitrogen, the
2 first isotope is nitrogen-14, and the second isotope is nitrogen-15.
- 1 61. The computer-readable medium of Claim 48, wherein the step of determining
2 whether the data indicates the occurrence of the mass doublet is based on input from a
3 user.
- 1 62. The computer-readable medium of Claim 48, wherein the instructions for determining
2 whether the data indicates the occurrence of the mass doublet further comprise
3 instructions which, when executed by one or more processors, cause the one or more
4 processors to carry out the steps of:
5 determining whether the data indicates that the mixture includes both the first version
6 of the polymer and the second version of the polymer;
7 determining whether both a first amount of the first version and a second amount of
8 the second version satisfy a first condition;
9 determining whether a ratio of the first amount to the second amount satisfies a
10 second condition; and
11 determining that the data indicates the occurrence of the mass doublet when the data
12 indicates that the mixture includes both the first version and the second
13 version, the first amount and the second amount satisfy the first condition, and
14 the ratio satisfies the second condition.

63. The computer-readable medium of Claim 62, wherein the first amount and the second amount satisfy the first condition when the first amount and the second amount exceed a threshold amount.

64. The computer-readable medium of Claim 62, wherein the ratio satisfies the second condition when the ratio is within a range based on a specified ratio and a specified error.

65. The computer-readable medium of Claim 48, wherein the data is based on multiple scans of a chromatogram of the mixture, and wherein the instructions for determining whether the data indicates an occurrence of the mass doublet further comprise instructions which, when executed by one or more processors, cause the one or more processors to carry out the steps of:
identifying, for each scan of a plurality of the multiple scans, whether the data indicates the occurrence of the mass doublet; and
if the data for a scan indicates the occurrence of the mass doublet, then generating a first value for said scan.

66. The computer-readable medium of Claim 65, wherein the first value is based on a first abundance of the first version and a second abundance of the second version.

67. The computer-readable medium of Claim 65, wherein the instructions for determining whether the data indicates an occurrence of the mass doublet further comprise instructions which, when executed by one or more processors, cause the one or more processors to carry out the steps of:
determining a number of consecutive scans of the plurality of the multiple scans for which a first value is generated; and

if the number of consecutive scans satisfies a specified condition, generating a second value.

68. The computer-readable medium of Claim 67, wherein the instructions for determining whether the data indicates an occurrence of the mass doublet further comprise instructions which, when executed by one or more processors, cause the one or more processors to carry out the steps of:
if the data indicates the occurrence of the mass doublet, associating the second value with the polymer.

69. The computer-readable medium of Claim 67, wherein the number of consecutive scans satisfies the specified condition when the number of consecutive scans is at least as great as a specified number of scans.

70. The computer-readable medium of Claim 67, wherein the second value is based on the first values that are associated with the number of consecutive scans.

71. The computer-readable medium of Claim 67, further comprising instructions which, when executed by the one or more processors, cause the one or more processors to carry out the step of:
determining a quantity measurement based on the second value.

72. The computer-readable medium of Claim 48, further comprising instructions which, when executed by the one or more processors, cause the one or more processors to carry out the step of:
automatically determining a quantity measurement for the polymer.

73. The computer-readable medium of Claim 72, wherein the quantity measurement is a qualitative measurement.

- 1 74. The computer-readable medium of Claim 72, wherein the quantity measurement is a
2 relative quantity measurement.
- 1 75. The computer-readable medium of Claim 72, wherein the quantity measurement is an
2 absolute quantity measurement
- 1 76. The computer-readable medium of Claim 48, wherein the instructions for generating
2 both the first mass and the second mass further comprise instructions which, when
3 executed by one or more processors, cause the one or more processors to carry out the
4 steps of:
5 calculating the first mass based on a first theoretical mass for the first version of the
6 polymer; and
7 calculating the second mass based on a second theoretical mass for the second version
8 of the polymer.
- 1 77. A computer-readable medium carrying one or more sequences of instructions for
2 identifying a polymer in a mixture, wherein execution of the one or more sequences
3 of instructions by one or more processors causes the one or more processors to
4 perform the steps of:
5 receiving one or more length values for fragments of the polymer;
6 based on the one or more length values, generating a library of fragments of the
7 polymer that have lengths corresponding to the one or more length values; and
8 for each fragment in the library, determining whether said fragment is present in the
9 mixture based on a mass spectrographic analysis of the mixture.
- 1 78. The computer-readable medium of Claim 77, wherein the one or more length values
2 includes a minimum length.

- 1 79. The computer-readable medium of Claim 77, wherein the one or more length values
2 includes a maximum length.
- 1 80. The computer-readable medium of Claim 77, wherein the one or more length values
2 includes a minimum length and a maximum length.
- 1 81. The computer-readable medium of Claim 77, wherein the one or more length values
2 includes one or more ranges of lengths.
- 1 82. The computer-readable medium of Claim 77, wherein the one or more length values
2 includes a one or more specified length values that are received from a user.
- 1 83. The computer-readable medium of Claim 77, wherein the instructions for determining
2 further comprise instructions which, when executed by one or more processors, cause
3 the one or more processors to carry out the steps of:
4 for each fragment in the library, generating both a first mass based on the fragment
5 having a first isotope of an element and a second mass based on the fragment
6 having a second isotope of the element;
7 for each fragment in the library, determining whether the mass spectrographic
8 analysis indicates an occurrence of a mass doublet that is associated with both
9 the first mass and the second mass.
- 1 84. A computer-readable medium carrying one or more sequences of instructions for
2 detecting biopolymers in a mixture that includes both natural and labeled versions of
3 the biopolymers, wherein execution of the one or more sequences of instructions by
4 one or more processors causes the one or more processors to perform the steps of:
5 generating a library for at least one biopolymer, wherein the library includes a
6 plurality of biopolymer fragments based on the at least one biopolymer;

7 determining, for each biopolymer fragment of the plurality of biopolymer fragments,
8 both a first mass based on a natural version of the biopolymer fragment that
9 includes a first isotope of an element and a second mass based on a labeled
10 version of the biopolymer fragment that includes a second isotope of the
11 element;
12 receiving information based on a mass spectrographic analysis of a chromatogram of
13 the mixture, wherein the information includes data for a plurality of scans of
14 the chromatogram;
15 identifying, for each scan of the plurality of scans, whether the data indicates an
16 occurrence of one or more mass doublets, wherein each mass doublet of the
17 one or more mass doublets is associated with both the natural version and the
18 labeled version of a particular biopolymer fragment of the plurality of
19 biopolymer fragments;
20 for each mass doublet that is identified,
21 generating a first score for each scan;
22 determining a number of consecutive scans of the plurality of scans for which
23 the first score is generated;
24 if the number of consecutive scans satisfies a specified condition, generating a
25 second score; and
26 associating the second score with the particular biopolymer fragment that is
27 associated with the mass doublet.

- 1 85. The computer-readable medium of Claim 84, further comprising instructions which,
2 when executed by the one or more processors, cause the one or more processors to
3 carry out the steps of:
4 receiving input that specifies a particular number of scans; and

wherein the number of consecutive scans satisfies the specified condition when the number of consecutive scans is at least as great as the particular number of scans.

86. The computer-readable medium of Claim 84, wherein the instructions for identifying, for each scan of the plurality of scans, whether the data indicates the occurrence of one or more mass doublets further comprise instructions which, when executed by one or more processors, cause the one or more processors to carry out the steps of: for each mass doublet of the one or more mass doublets, determining whether the data indicates that the mixture includes both the natural version and the labeled version of the particular biopolymer fragment; determining whether both a first abundance of the natural version and a second abundance of the labeled version exceed a threshold abundance; and determining whether a ratio of the first abundance of the natural version to the second abundance of the labeled version is consistent with both a specified ratio and a specified error; and identifying that the data indicates the occurrence of the mass doublet when the data indicates that the mixture includes both the natural version and the labeled version, the first abundance and the second abundance exceed the threshold abundance, and the ratio is consistent with both the specified ratio and the specified error.

87. The computer-readable medium of Claim 86, further comprising instructions which, when executed by the one or more processors, cause the one or more processors to carry out the steps of:

receiving input that specifies a mass/charge accuracy associated with the mass spectrographic analysis; and wherein the step of determining whether the data indicates that mixture includes both the natural version and the labeled version of the particular biopolymer fragment comprises the computer-implemented step of: identifying whether a first peak occurs in the data, wherein the first peak is based on the first mass and the mass/charge accuracy; identifying whether a second peak occurs in the data, wherein the second peak is based on the second mass and the mass/charge accuracy; and determining that the data indicates that the mixture includes both the natural version and the labeled version of the particular biopolymer fragment when both the first peak and the second peak occur in the data.

88. The computer-readable medium of Claim 84, wherein the instructions for determining both the first mass based on the natural version of the biopolymer fragment and the second mass based on the labeled version of the biopolymer fragment further comprise instructions which, when executed by one or more processors, cause the one or more processors to carry out the steps of: calculating the first mass based on a first theoretical mass for the natural version of the biopolymer fragment; and calculating the second mass based on a second theoretical mass for the labeled version of the biopolymer fragment.

89. The computer-readable medium of Claim 88, further comprising instructions which, when executed by the one or more processors, cause the one or more processors to carry out the steps of:

repeating the steps of calculating the first mass and calculating the second mass for
each possible charge state of the biopolymer fragment.

90. The computer-readable medium of Claim 89, further comprising instructions which,
when executed by the one or more processors, cause the one or more processors to
carry out the steps of:
receiving input that specifies one or more possible charge states of the biopolymer
fragment.

91. The computer-readable medium of Claim 84, wherein the instructions for generating
the first score further comprise instructions which, when executed by one or more
processors, cause the one or more processors to carry out the steps of:
calculating the first score as a sum of a first average abundance that corresponds to
the first mass and a second average abundance that corresponds to the second
mass.

92. The computer-readable medium of Claim 84, wherein the instructions for generating
the second score further comprise instructions which, when executed by one or more
processors, cause the one or more processors to carry out the steps of:
calculating the second score as a summation of each first score associated with each
of the number of consecutive scans.

93. The computer-readable medium of Claim 84, further comprising instructions which,
when executed by the one or more processors, cause the one or more processors to
carry out the step of:
ranking, based on the second score for each biopolymer fragment, the one or more
mass doublets that are identified.

- 1 94. The computer-readable medium of Claim 84, further comprising instructions which,
- 2 when executed by the one or more processors, cause the one or more processors to
- 3 carry out the step of:
- 4 displaying a plot as a function of time of both a first abundance of the first mass and a
- 5 second abundance of the second mass.